Amendments in the Specification

Please delete the text inserted on page 5, after line 12, in the reply dated July 2, 2002. The text to be deleted recites:

-- The HPT1, hPEPT1, D2H, and hSI receptors were selected for cloning as GIT receptor targets based on several criteria, including: (1) expression on surface of epithelial cells in gastro-intestinal tract (GIT); (2) expression along the length of small intestine (HPT1, hPEPT1, D2H); (3) expression locally at high concentration (hSI); (4) large putative extracellular domains facing into the lumen of the GIT; and (5) extracellular domains that permit easy access and bioadhesion by targeting particles.

The four recombinant receptor sites screened with the peptide libraries additionally have the following characteristics:

sucrose and other sugars, represents 9% of brush border membrane protein in

Receptor	<u>Characteristics</u>
D2H	Transport of neutral/basic amino acids; a transport
	activating protein for a range of amino acid translocases
hSI	Metabolism of sucrose and other sugars, represents 9% of
	brush border membrane protein in Jejunum
HPT1	di/tri peptide transporter or facilitator of peptide transport
hPEPT1	di/tri peptide transporter

6.2 Cloning of Extracellular Domain of Selected Receptor Site

The following receptor domains were cloned and expressed as His-tag fusion proteins by standard techniques:

Receptor	Domain (amino
·	acid residues)

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hPEPT1*	391-571
HPT1 ^b	29-273
hSIe	272-667
D2H ^t	387-685

- a Liang et al., 1995, J. Biol. Chem. 270: 6456-6463;
- b Dantzig et al., 1994, Association of Intestinal Peptide Transport with a Protein Related to the Cadherin Superfamily;
- c Chantret et al., Biochem. J. 285: 915-923;
- d Bertran et al., J. Biol. Chem. 268: 14842-14949.

The receptor proteins were expressed as His-tag fusion proteins and affinity purified under denaturing conditions, using urea or guanidine HCl, utilizing the pET His-tag metal chelate affinity for Ni-NTA Agarose (Hochuli, E., Purification of recombinant proteins with metal chelate adsorbent, Genetic Engineering, Principals and Methods (J.K. Setlow, ed.), Plenum Press, NY, Vol. 12 (1990), pp. 87-98).

As indicated in WO 98/51325, phage which showed specificity to a GIT receptor was further characterized by ELISA on a variety of recombinant proteins. Phage which continued to exhibit GIT receptor specificity was sequenced. Their insert sequences are summarized as follows:

	EQ.
<u>hSI</u>	D.NO TARGET BINDING PHAGE INSERT SEQUENCE
S15	6. RSGAYESPDGRGGRSYVGGGGGGGGNIGRKIINLWGLRTASPACWD
S21	7. SPRSFWPWSRHESFGISNYLGCGYRTCISGTMTKSSPIYPRHS

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S22	18.	-SSSDWGGVPGKWRERFKGRGCGISITSVLTGKPNPCPEPKAA
Sni 10	19.	-RVGQCTDSDVRRPWARSCAHQGCGAGTRNSHGCITRPLRQASAH
Sni28	-20.	SHSGGMNRAYGDVFRELRDRWNATSHHTRPTPQLPRGPN
Sni34	21.	SPCGGSWGRFMQGGLFGGRTDGCGAHRNRTSASLEPPSSDY
Sni38	22.	-RGAADQRRGWSENLGLPRVGWDAIAHNSYTFTSRRPRPP
Sni45	23. —	-SGGEVSSWGRVNDLCARVSWTGCGTARSARTDNKGFLPKHSSLR
SniAX2	24.	SDSDGDHYGLRGGVRCSLRDRGCGLALSTVHAGPPSFYPKLSSP
SniAX4	25.	RS LGNYGVTGTVDVTVLPMPGHANHLGVSSASSSDPPRR
SniAX6	26 .	RTTTAKGCLLGSFGVLSGCSFTPTSPPPHLGYPPHSVN
SniAX8	27.	SPKLSSVGVMTKVTELPTEGPNAISIPISATLGPRNPLR
D2H		
DAB3	28.	-RWCGAELCNSVTKKFRPGWRDHANPSTHHRTPPPSQSSP
DAB7	29.	RWCGADDPCGASRWRGGNSLFGCGLRCSAAQSTPSGRIHSTSTS
DAB10	30.	-SKSGEGGDSSRGETGWARVRSHAMTAGRFRWYNQLPSDR
DAB18	31.	-RSSANNCEWKSDWMRRACIARYANSSGPARAVDTKAAP
DAB24	32.	SKWSWSSRWGSPQDKVEKTRAGCGGSPSSTNCHPYTFAPPPQAG
DAB30	33.	SGFWEFSRGLWDGENRKSVRSGCGFRGSSAQGPCPVTPATIDKH
DAM 5	34.	SESGRCRSVSRWMTTWQTQKGGCGSNVSRGSPLDPSHQTGHATT
DAX23	35.	REWRFAGPPLDLWAGPSLPSFNASSHPRALRTYWSQRPR
DAX24	36.	RMEDIKNSGWRDSCRWGDLRPGCGSRQWYPSNMRSSRDYPAGGII
DAX27	37.	SHPWYRHWNHGDFSGSGQSRHTPPESPHPGRPNATI
DCX8	38.	RYKHDIGCDAGVDKKSSSVRGGCGAHSSPPRAGRGPRGTMVSRL
DCX11	39 .	SQGSKQCMQYRTGRLTVGSEYGCGMNPARHATPAYPARLLPRYR
DCX26	40 .	SGRTTSEISGLWGWGDDRS GYGWGNTLRPNYIPYRQATNRIIRYT
DCX33	41.	RWNWTVLPATGGHYWTRSTDYHAINNHRPSIPHQHPTPI
DCX36	-42	SWSSWNWSSKTTRLGDRATREGCGPSQSDGCPYNGRLTTVKPRT
DCX39	43.	SGSLNAWQPRSWVGGAFRSHANNNLNPKPTMVTRHPT
DCX42	44.	RYSGLSPRDNGPACSQEATLEGCGAQRLMSTRRKGRNSRPGWTL
DCX45	45.	-SVGNDKTSRPVSFYGRVSDLWNASLMPKRTPSSKRIIDDG

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hPEPT1

PAX9	46	
PAX14	47.	RTFENDGLGVGRSIQKKSDRWYASHNIRSHFASMSPAGK
PAX15	48.	SYCRVKGGGEGGHTDSNLARSGCGKVARTSRLQHINPRATPPSR
PAX16	49.	- SWTRWGKHTHGGFVNKSPPGKNATSPYTDAQLPSDQGPP
PAX17	-50.	SQVDSFRNSFRWYEPSRALCHGCGKRDTSTTRHINSPSDSYPTR
PAX18	5 1.	
PAX35	52.	RSITDGGINEVDLSSVSNVLENANSHRAYRKHRPTLKRP
PAX38	53 .	SSKVSSPRDPTVPRKGGNVDYGCGHRSSARMPTSALSSITKCYT
PAX40	-54.	RASTQGGRGVAPEFGASVLGRGCGSATYYTNSTSCKDAMGHNYS
PAX43	-55. -	
PAX45	-56.	SFQVYPDHGLERHALDGTGPLYAMPGRWIRARPQNRDRQ
PAX46	57.	
P31	58.	SARDSGPAEDGSRAVRLNGVENANTRKSSRSNPRGRRHP
P90	59 .	SSADAEKCAGSLLWWGRQNNSGCGSPTKKIILKIIRNRSQTSSSSII
5PAX3	-60.	
5PAX5	61.	RGSTGTAGGERSGVLNLHTRDNASGSGFKPWYPSNRGHK
5PAX7	-62. -	RWGWERSPSDYDSDMDLGARRYATRTHRAPPRVLKAPLP

HPT-1

5PAX12 63.

HAX9	64.	- SREEANWDGYKREMSHRSRFWDATHLSRPRRPANSGDPN
HAX35	-65.	-EWYSWKRSSKSTGLGDTATREGCGPSQSDGCPYNGRLTTVKPRK
HAX40	-66	REFAERRLWGCDDLSWRLDAEGCGPTPSNRAVKHRKPRPRSPAL
HAX42	-67	SDHALGTNLRSDNAKEPGDYNCCGNGNSTGRKVFNRRRPSAIPT
HCA3	-68.	RHISEYSFANSHLMGGESKRKGCGINGSFSPTCPRSPTPAFRRT
H40	-69.	SRESGMWGSWWRGHRLNSTGGNANMNASLPPDPPVSTP
PAX2	70.	STPPSREAYSRPYSVDSDSDTNAKHSSHNRRLRTRSRPN-

RGWKCEGSQAAYGDKDIGRSRGCGSITKNNTNHAHPSHGAVAKI

Synnestvedt & Lechner Llp

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Please delete the text inserted on page 6, after line 14, in the reply dated July 2, 2002. The text to be deleted recites:

--In a specific embodiment of the invention, proteins consisting of or, alternatively, comprising all or a fragment of a GIT transport receptor-binding peptide consisting of at least 5, 10, 15, 20, 25, 30 or 35 (contiguous) amino acids of the full-length GIT transport receptor-binding peptide are provided. In a specific embodiment, such proteins are not more than 20, 30, 40, 50, or 75 amino acids in length. Derivatives or analogs of GIT transport receptor-binding peptides include but are not limited to those molecules comprising regions that are substantially homologous to GIT transport receptor-binding peptides or fragments thereof (e.g., at least 50%, 60%, 70%, 80% or 90% identity) (e.g., over an identical size sequence or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art) or whose encoding nucleic acid is capable of hybridizing to a coding GIT transport receptor-binding peptide sequence, under stringent, moderately stringent, or nonstringent conditions.--